
DNA Barcoding Evolves into the Familiar

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A Place for Barcodes

First, there is nothing wrong with careful use of a DNA barcode to help identify an unknown specimen; indeed, in some cases, it might be the most effective way to find a name for many species. The caveat is that the unknown specimen needing identification is from a previously described (known to science) species. Problems arise when the unknown specimen comes from the majority of biodiversity that is undescribed, and the barcode becomes the only data by which the species is understood. This is unlikely to be the case for most vertebrates or many plants because most species are already known. Although there are special cases in which a life stage or body part is difficult to identify to species (DeSalle & Birstein 1996; Rubinoff 2006), many vertebrate and plant specimens may be identifiable without a need for DNA. For specific uses such as quarantine against known insect pests, barcodes could be invaluable for speed and accuracy.

Nevertheless, the biodiversity crisis is the rapid loss of species, especially those that have never been identified, described, or studied. They are the great unknown, the "taxonomic impediment" to understanding and preserving biodiversity, and at least part of the rationale for the initial barcoding proposals (Hebert et al. 2003). Many, if not most, of these unknown species are insects, the bulk of this planet's biodiversity. Therefore, finding barcodes for previously described species is not going to address these unknown species and help us understand the scope or scale of the biodiversity crisis. There is nothing inherently wrong with having barcodes for previously identified species, if the DNA sequences are properly analyzed (DeSalle et al. 2005). But generating barcodes for known species is not the best way to conserve the vast number of unknown, never-identified species. I suggest such a practice is akin to tidying one's room while the house is on fire.

Integrated Barcodes

DeSalle and I agree on a wide range of barcoding aspects, although we may agree on more issues than I might with other proponents of barcoding (e.g., species discovery vs. identification and character-based analysis). My phrase *identifying new species* has the same meaning as DeSalle's *species discovery*, and my opposition is to the practice by which species are known and identifiable only through a DNA barcode (first paragraph of "Conclusion," Rubinoff 2006). The "different light" in which DeSalle suggests we view barcoding includes fundamental changes in the way barcoders function, and sound theoretical boundaries for their application. This is not a different light, it is a whole new sun. The extreme makeover includes the use of evolution-based rather than distance-based methods of tree construction that would greatly improve the methodology and its usefulness. Furthermore, the brand of barcoding DeSalle advocates is quite different from earlier proposals (e.g., Hebert et al. 2003) and incorporates an "integrated" approach that I and others have also advocated repeatedly (Dayrat 2005; Rubinoff & Holland 2005; Will et al. 2005; Rubinoff 2006; Rubinoff et al. 2006).

I suggest that as more participants have become involved in the barcoding debate, the procedure termed *barcoding* has evolved for the better. My essay is a commentary on the barcoding paradigm cited therein. A process like that advocated by DeSalle in this issue and in DeSalle et al. (2005) is a fine response to concerns I and others raised to earlier barcoding models. The use of multiple sources of data, including DNA, in a character-based analysis to come up with fast identifications is something I advocate (Rubinoff 2006). There are a few, smaller points on which DeSalle and I may disagree concerning the practical application of barcodes for the general public (see Cameron et al. 2006), but on the broad issues things are

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much improved. Whether others will follow this new model for barcoding remains to be seen. I propose the term *integrated barcodes* for the identification tool DeSalle and I discuss here because it reflects the possible inclusion of nuclear DNA, ecological, and/or morphological data with mtDNA sequence—which was not part of the original DNA barcode.

Hebert et al. (2004) conducted a fine study that provides a good example of delving into unknown biodiversity through the use of morphology, ecology, and DNA, but their work is not barcoding. If it is, barcoding has been around since DNA was first used in systematics, and I myself am happily guilty of such a practice (Rubinoff & Powell 2004; Rubinoff & Sperling 2004). All these studies use integrated data sets that, in addition to not being new, are not going to save the time needed to help identify global biodiversity before it disappears. Even the suggestion that molecular workers focus on the same region of mtDNA was suggested before barcoding became a common term (Caterino et al. 2000). So if barcodes solely are to mean the use of mtDNA to get a name for a specimen of a species, which has already been described on the basis of the integrated data sets, I see relatively few problems (for an example of such a problem, see Omland et al. 2006).

But such a system begs the question: what's new? Barcoding gathered momentum quickly because its early proponents bemoaned the slow pace of taxonomy to quantify global biodiversity (Hebert et al. 2003) and sought a faster, better way. But barcodes that use, or at least rely on studies that use, multiple sources of data—although commendably accurate—are going to take much longer than original estimates to quantify global biodiversity. It is not going to be as simple as churning specimens through a DNA sequencer. This then might be the only point on which DeSalle and I seem to disagree: the boon an integrated barcode would represent to global biodiversity assessments. Because some knowledge of species is needed to describe them, this process will continue to be slow, and the pace of taxonomic discovery would not seem to be greatly increased by barcodes per se.

As is the case with any productive debate, some points of agreement seem to have been reached. I appreciate DeSalle's (2006 [this issue]) reference to our statement (Rubinoff & Holland 2005) regarding babies and bathwater. The challenge will be the designation of minimum standards for baseline data so that barcodes do not become bathwater. Perhaps most researchers now agree that barcoding should not mean the sole use of mtDNA to identify (discover) new species and understand global biodiversity (see <http://phe.rockefeller.edu/barcode/blog/>). Barcodes are simply a shorthand method for identifying previously described and characterized taxa. We concur that integrated data sets, including DNA, morphology, and

ecology, are essential to understanding global biodiversity and should be used in an evolution-based barcoder (DeSalle et al. 2005). With such agreements, it is to be hoped that we can increase the pace of productive collaborations between those with appropriate expertise in molecular, morphological, and ecological methods and, united in concerted efforts, continue with the business of quantifying global biodiversity.

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